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RAW SEQUENCE LISTING   DATE: 04/05/2001
PATENT APPLICATION: US/09/669,476   TIME: 08:23:48

Input Set : A:\ES.txt
Output Set: N:\CRF3\04052001\I669476.raw

SEQUENCE LISTING

```
   4 (1) GENERAL INFORMATION:
   6      (i) APPLICANT: Botella, Jose Ramon
   8     (ii) TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
  10    (iii) NUMBER OF SEQUENCES: 19
  12     (iv) CORRESPONDENCE ADDRESS:
  13          (A) ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
  14          (B) STREET: 100 Thanet Circle, Suite 306
  15          (C) CITY: Princeton
  16          (D) STATE: NJ
  17          (E) COUNTRY: USA
  18          (F) ZIP: 08540-3662
  20      (v) COMPUTER READABLE FORM:
  21          (A) MEDIUM TYPE: Floppy disk
  22          (B) COMPUTER: IBM PC compatible
  23          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  24          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
  26     (vi) CURRENT APPLICATION DATA:
C--> 27          (A) APPLICATION NUMBER: US/09/669,476
C--> 28          (B) FILING DATE: 25-Sep-2000
  29          (C) CLASSIFICATION:
  39    (vii) PRIOR APPLICATION DATA:
  32          (A) APPLICATION NUMBER: PCT/AU96/00591
  33          (B) FILING DATE: 20-SEP-1996
  36          (A) APPLICATION NUMBER: AU PN5559
  37          (B) FILING DATE: 20-SEP-1995
  40          (A) APPLICATION NUMBER: AU PN9603
  41          (B) FILING DATE: 02-MAY-1996
  43   (viii) ATTORNEY/AGENT INFORMATION:
  44          (A) NAME: Bernstein, Scott N.
  45          (B) REGISTRATION NUMBER: 38,827
  46          (C) REFERENCE/DOCKET NUMBER: 3573-11US
  48     (ix) TELECOMMUNICATION INFORMATION:
  49          (A) TELEPHONE: 609-924-8555
  50          (B) TELEFAX: 609-924-3036
  53 (2) INFORMATION FOR SEQ ID NO: 1:
  55      (i) SEQUENCE CHARACTERISTICS:
  56          (A) LENGTH: 1080 base pairs
  57          (B) TYPE: nucleic acid
  58          (C) STRANDEDNESS: single
  59          (D) TOPOLOGY: linear
  61     (ii) MOLECULE TYPE: cDNA
  64     (ix) FEATURE:
  65          (A) NAME/KEY: CDS
  66          (B) LOCATION: 1..1080
  69     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
  71 CAG ATG GGG TTT GCG GAG AAC CAG CTT TCG CTG GAG TTA ATA CGT GAG          48
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72 Gln Met Gly Phe Ala Glu Asn Gln Leu Ser Leu Glu Leu Ile Arg Glu
73  1               5                   10                  15
75 TGG ATC AAG AAT CAC CCG GAG GCC TCC ATT TGC TCG GCG GAG GGC CTG      96
76 Trp Ile Lys Asn His Pro Glu Ala Ser Ile Cys Ser Ala Glu Gly Leu
77              20                  25                  30
79 CCG CAG TTC ATG GAG ATC GCC AAT TTC CAA GAC TAC CAT GGC TTG CCG      144
80 Pro Gln Phe Met Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro
81          35                  40                  45
83 GCT TTT CTG CAG GGA ATC GCG AAA TTG ATG GAG AAA GTG AGA GGA GGA      192
84 Ala Phe Leu Gln Gly Ile Ala Lys Leu Met Glu Lys Val Arg Gly Gly
85          50                  55                  60
87 AGG GTC AAA TTC GAT CCG AAC CGC GTG GTG ATG AGC GGC GGA GGC ACT      240
88 Arg Val Lys Phe Asp Pro Asn Arg Val Val Met Ser Gly Gly Gly Thr
89  65                  70                  75                  80
91 GGA GCG CAA GAA ACG CTC GCG TTT TGT CTC GCT GAC CCT GGC GAC GCC      288
92 Gly Ala Gln Glu Thr Leu Ala Phe Cys Leu Ala Asp Pro Gly Asp Ala
93              85                  90                  95
95 TTC CTC GTC CCA ACT CCG TAC TAT CCA GCA TTT AAT CGC GAT CTC CGG      336
96 Phe Leu Val Pro Thr Pro Tyr Tyr Pro Ala Phe Asn Arg Asp Leu Arg
97              100                 105                 110
99 TGG AGA ACG GGC GTC GAG CTC CTC CCG GTT CAC TGC AAG AGC TCT AAT      384
100 Trp Arg Thr Gly Val Glu Leu Leu Pro Val His Cys Lys Ser Ser Asn
101          115                 120                 125
103 CAC TTC AGA GTC ACC AAA ACG GCG CTA GAA TCG GCA TAC GAG AAG GCG     432
104 His Phe Arg Val Thr Lys Thr Ala Leu Glu Ser Ala Tyr Glu Lys Ala
105          130                 135                 140
107 CGA AAG GAT AAC ATC AGA GTA AAA GGA GTA CTG ATA ACC AAC CCA TCC     480
108 Arg Lys Asp Asn Ile Arg Val Lys Gly Val Leu Ile Thr Asn Pro Ser
109 145                 150                 155                 160
111 AAC CCG CTC GGC ACG ACC ATG GAT AAA CAC ACG CTA CAG ACC CTC GTG     528
112 Asn Pro Leu Gly Thr Thr Met Asp Lys His Thr Leu Gln Thr Leu Val
113              165                 170                 175
115 AAA TTC GTA AAC GAA AGG AGA ATC CAC CTA GTC TGC GAC GAG TTA TAC     576
116 Lys Phe Val Asn Glu Arg Arg Ile His Leu Val Cys Asp Glu Leu Tyr
117              180                 185                 190
119 GGC GCA ACC ATC TTT AGG GAG CCC AGG TTC GTC AGC ATC TCC GAG GTA     624
120 Gly Ala Thr Ile Phe Arg Glu Pro Arg Phe Val Ser Ile Ser Glu Val
121          195                 200                 205
123 ATA GAA GAG GAC CCG AAC TGC GAC AAG AAT CTG ATC CAC ATT GCG TAC     672
124 Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr
125          210                 215                 220
127 AGT CTC TCA AAG GAC TTC GGT CTC CCC GGA TTC CGA GTC GGG ATC GTG     720
128 Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val
129 225                 230                 235                 240
131 TAT TCC TAC AAC GAC ACG GTG GTT AGT TGC GCA CGC AGA ATG TCG AGC     768
132 Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser
133              245                 250                 255
135 TTC GGC CTC GTC TCG TCG CAG ACA CAG TAC CTA CTG GCC GCC ATG CTA     816
136 Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu
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```
137              260               265                270
139 TCC GGC GAA GAA TTT TTG CCA ACA TTA CTG ACT GAA AGC GCG AAG AGT        864
140 Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser
141          275               280                285
143 CTG TCG GAG AGC CAC AGG ATC TTC TCT TCC GGC CTT GAG GAA GTC GAC        912
144 Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp
145          290               295               300
147 ATC CGC TGC TTG GAC GGC AAT GCC GGG GTC TTC TGC TGG ATG GAC CTA        960
148 Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu
149 305               310               315               320
151 CGG CAC CTC CTC AAA GAA GCC ACC GAA GAC GGC GAG CTC GAG CTG TGG       1008
152 Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp
153          325               330               335
155 CGC GTG ATA GTG AAC AAT GTC AAG CTC AAT GTG TCC CCC GGT TCG TCG       1056
156 Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser
157          340               345               350
159 TTT TAT TGC GCC GAG CCA GGT TGG                                       1080
160 Phe Tyr Cys Ala Glu Pro Gly Trp
161          355               360
164 (2) INFORMATION FOR SEQ ID NO: 2:
166      (i) SEQUENCE CHARACTERISTICS:
167          (A) LENGTH: 360 amino acids
168          (B) TYPE: amino acid
169          (D) TOPOLOGY: linear
171      (ii) MOLECULE TYPE: protein
173      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
175 Gln Met Gly Phe Ala Glu Asn Gln Leu Ser Leu Glu Leu Ile Arg Glu
176  1              5                   10                  15
178 Trp Ile Lys Asn His Pro Glu Ala Ser Ile Cys Ser Ala Glu Gly Leu
179           20                  25                  30
181 Pro Gln Phe Met Glu Ile Ala Asn Phe Gln Asp Tyr His Gly Leu Pro
182           35                  40                  45
184 Ala Phe Leu Gln Gly Ile Ala Lys Leu Met Glu Lys Val Arg Gly Gly
185      50                  55                  60
187 Arg Val Lys Phe Asp Pro Asn Arg Val Val Met Ser Gly Gly Gly Thr
188  65               70                  75                  80
190 Gly Ala Gln Glu Thr Leu Ala Phe Cys Leu Ala Asp Pro Gly Asp Ala
191              85                  90                  95
193 Phe Leu Val Pro Thr Pro Tyr Tyr Pro Ala Phe Asn Arg Asp Leu Arg
194           100                 105                 110
196 Trp Arg Thr Gly Val Glu Leu Leu Pro Val His Cys Lys Ser Ser Asn
197           115                 120                 125
199 His Phe Arg Val Thr Lys Thr Ala Leu Glu Ser Ala Tyr Glu Lys Ala
200      130                 135                 140
202 Arg Lys Asp Asn Ile Arg Val Lys Gly Val Leu Ile Thr Asn Pro Ser
203 145               150                 155                 160
205 Asn Pro Leu Gly Thr Thr Met Asp Lys His Thr Leu Gln Thr Leu Val
206              165                 170                 175
208 Lys Phe Val Asn Glu Arg Arg Ile His Leu Val Cys Asp Glu Leu Tyr
```

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```
209              180                185                190
211 Gly Ala Thr Ile Phe Arg Glu Pro Arg Phe Val Ser Ile Ser Glu Val
212          195                200                205
214 Ile Glu Glu Asp Pro Asn Cys Asp Lys Asn Leu Ile His Ile Ala Tyr
215      210                215                220
217 Ser Leu Ser Lys Asp Phe Gly Leu Pro Gly Phe Arg Val Gly Ile Val
218 225                230                235                240
220 Tyr Ser Tyr Asn Asp Thr Val Val Ser Cys Ala Arg Arg Met Ser Ser
221              245                250                255
223 Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Leu Ala Ala Met Leu
224          260                265                270
226 Ser Gly Glu Glu Phe Leu Pro Thr Leu Leu Thr Glu Ser Ala Lys Ser
227      275                280                285
229 Leu Ser Glu Ser His Arg Ile Phe Ser Ser Gly Leu Glu Glu Val Asp
230      290                295                300
232 Ile Arg Cys Leu Asp Gly Asn Ala Gly Val Phe Cys Trp Met Asp Leu
233 305                310                315                320
235 Arg His Leu Leu Lys Glu Ala Thr Glu Asp Gly Glu Leu Glu Leu Trp
236              325                330                335
238 Arg Val Ile Val Asn Asn Val Lys Leu Asn Val Ser Pro Gly Ser Ser
239          340                345                350
241 Phe Tyr Cys Ala Glu Pro Gly Trp
242      355                360
244 (2) INFORMATION FOR SEQ ID NO: 3:
246      (i) SEQUENCE CHARACTERISTICS:
247          (A) LENGTH: 1104 base pairs
248          (B) TYPE: nucleic acid
249          (C) STRANDEDNESS: single
250          (D) TOPOLOGY: linear
252      (ii) MOLECULE TYPE: cDNA
255      (ix) FEATURE:
256          (A) NAME/KEY: CDS
257          (B) LOCATION: 1..1104
260      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
262 CAG ATG GGC CTT GCT GAG AAT CAG CTT TGC TTT AAT TTA ATT CAC GAG        48
263 Gln Met Gly Leu Ala Glu Asn Gln Leu Cys Phe Asn Leu Ile His Glu
264  1              5                10                15
266 TGG CCG CTG AAA AAC CCA GAA GCC TCC ATT TGT ACA ACA CAA GGA GCA        96
267 Trp Pro Leu Lys Asn Pro Glu Ala Ser Ile Cys Thr Thr Gln Gly Ala
268          20                25                30
270 GCT GAA TTC AGA GAT ATA GCT ATC TTT CAA GAT TAT CAT GGC TTG GCT       144
271 Ala Glu Phe Arg Asp Ile Ala Ile Phe Gln Asp Tyr His Gly Leu Ala
272          35                40                45
274 GAA TTC AGA GAG GCT GTT GCA AAG TTT ATG GGG AAA GTG AGA AGA AAC       192
275 Glu Phe Arg Glu Ala Val Ala Lys Phe Met Gly Lys Val Arg Arg Asn
276      50                55                60
278 AGA GCT TCA TTT GAC CCT GAT CGG ATT GTT ATG AGT GGA GGA GCA ACT       240
279 Arg Ala Ser Phe Asp Pro Asp Arg Ile Val Met Ser Gly Gly Ala Thr
280  65                70                75                80
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```
282 GGA GCT CAT GAA ATG ATT GGT TTC TGT TTG GCT GAT CCT GGC GAT GCA        288
283 Gly Ala His Glu Met Ile Gly Phe Cys Leu Ala Asp Pro Gly Asp Ala
284             85                  90                  95
286 TTC TTG GTT CCA ACT CCT TAT TAT CCA GGG TTT GAT AGA GAT TTG AGA        336
287 Phe Leu Val Pro Thr Pro Tyr Tyr Pro Gly Phe Asp Arg Asp Leu Arg
288            100                 105                 110
290 TGG AGA ACG GGA GTC AAA CTC ATT CCA GTT GTC TGT GAA AGC TCA AAC        384
291 Trp Arg Thr Gly Val Lys Leu Ile Pro Val Val Cys Glu Ser Ser Asn
292         115                 120                 125
294 GAT TAC CAG ATC ACC ATA GAA GCC CTG GAA GCT GCT TAT GAA ACC GCA        432
295 Asp Tyr Gln Ile Thr Ile Glu Ala Leu Glu Ala Ala Tyr Glu Thr Ala
296      130                 135                 140
298 CAA GAA GCT GAC ATC AAG GTA AAG GGT TTG GTC ATA ACC AAC CCA TCA        480
299 Gln Glu Ala Asp Ile Lys Val Lys Gly Leu Val Ile Thr Asn Pro Ser
300 145                 150                 155                 160
302 AAC CCA CTG GGA ACA ATT ATT ACC AAG GAC ACA TTA GAA GCT CTA GTC        528
303 Asn Pro Leu Gly Thr Ile Ile Thr Lys Asp Thr Leu Glu Ala Leu Val
304             165                 170                 175
306 ACC TTC ACC AAC CAC AAG AAC ATT CAT CTG GTG TGT GAT GAG ATA TAT        576
307 Thr Phe Thr Asn His Lys Asn Ile His Leu Val Cys Asp Glu Ile Tyr
308             180                 185                 190
310 GCT GGT TAC CGT CTT CAG CCC AGG GCC GAA TTC ACC AGC ATA GCC GAG        624
311 Ala Gly Tyr Arg Leu Gln Pro Arg Ala Glu Phe Thr Ser Ile Ala Glu
312         195                 200                 205
314 ATA ATT GAA GAA GAT AAA ATT TGT TGC AAT CGT GAT CTC ATC CAC ATC        672
315 Ile Ile Glu Glu Asp Lys Ile Cys Cys Asn Arg Asp Leu Ile His Ile
316      210                 215                 220
318 ATT TAC AGT TTA TCC AAA GAC ATG GGA TTC CCT GGA TTT AGA GTT GGC        720
319 Ile Tyr Ser Leu Ser Lys Asp Met Gly Phe Pro Gly Phe Arg Val Gly
320 225                 230                 235                 240
322 ATT GTG TAT TCA TAC AAT GAT GCA GTG GTG AGT TGT GCT CGT AAG ATG        768
323 Ile Val Tyr Ser Tyr Asn Asp Ala Val Val Ser Cys Ala Arg Lys Met
324             245                 250                 255
326 TCG AGC TTC GGC CTA GTA TCT TCG CAA ACC CAG TAT CTG ATT GCA TCC        816
327 Ser Ser Phe Gly Leu Val Ser Ser Gln Thr Gln Tyr Leu Ile Ala Ser
328         260                 265                 270
330 ATG TTA GCA GAC GAT GAA TTT GTA GAC AAA TTT ATT GTA GAG AGC AGA        864
331 Met Leu Ala Asp Asp Glu Phe Val Asp Lys Phe Ile Val Glu Ser Arg
332         275                 280                 285
334 AAG AGG CTG GCA ATG AGA CAT AGT TTT TTC ACA CAA AGA CTT GCT CAA        912
335 Lys Arg Leu Ala Met Arg His Ser Phe Phe Thr Gln Arg Leu Ala Gln
336      290                 295                 300
338 GTA GGC ATT AAC TGT TTA AAA AGC AAT GCT GGT CTT TTT GTG TGG ATG        960
339 Val Gly Ile Asn Cys Leu Lys Ser Asn Ala Gly Leu Phe Val Trp Met
340 305                 310                 315                 320
342 GAT TTG CGT AGA CTG CTG AAA GAA CAG ACA TTT GAA GCA GAA ATG GTG       1008
343 Asp Leu Arg Arg Leu Leu Lys Glu Gln Thr Phe Glu Ala Glu Met Val
344             325                 330                 335
346 TTA TGG AGA GTA ATT ATA AAC GAA ATG AAA CTC AAT GTA TCT CCT GGT       1056
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VERIFICATION SUMMARY   DATE: 04/05/2001
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Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\04052001\I669476.raw**

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]